

015745-9.ST25.txt  
SEQUENCE LISTING

<110> LUKYANOV, SERGI A  
SHAGIN, DMITRY A  
YANUSHEVICH, YURY G

<120> FLUORESCENT PROTEINS AND CHROMOPROTEINS FROM NON-AEQUOREA  
HYDROZOA SPECIES AND METHODS FOR USING SAME

<130> U 015745-9

<140> 10/532,681

<141> 2005-04-26

<160> 22

<170> PatentIn version 3.3

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<212> DNA

<213> phialidium sp

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20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys  
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile  
85 90 95

Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe  
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
145 150 155 160

Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Glu Asp Phe  
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
180 185 190

Val His Val Pro Glu Tyr His His Ile Thr Tyr His Val Thr Leu Ser  
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val  
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
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<210> 3  
<211> 705  
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<223> phiYFP-Y1 mutant of the phiYFP

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gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atgggccaga attaaaggat      240
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<220>  
<223> phiYFP-Y1 mutant of the phiYFP

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35         40         45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50         55         60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65         70         75         80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
85         90         95

Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe

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100

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
145 150 155 160

Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
180 185 190

Val His Val Pro Glu Tyr His His Met Thr Tyr His Val Thr Leu Ser  
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val  
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
225 230

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<220>  
<223> phiYFP-M0 mutant of the phiYFP

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gtaacaacac ttacttatgg tgcacaatgc ttcgccaat atggtccaga attaaaggat 240  
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gacggaaact ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga 360  
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ttcaatttca cacctcattg tctttacatt tggggagatc aggctaataca tggtttgaag 480  
tctgctttca aaattcgcca tgagattact ggatcaaaag gagacttcat tgttcgagac 540  
cacacccaaa tgaacacacc cattggtggt ggaccagtc atgtccctga aaaccatcat 600

atgagctacc atgtcaagct cagcaaagat gttactgatac acagggataa catgagcttg 660  
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<223> phiYFP-M0 mutant of the phiYFP

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20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys  
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile  
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe  
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
145 150 155 160

Ser Ala Phe Lys Ile Arg His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
180 185 190

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Val His Val Pro Glu Asn His His Met Ser Tyr His Val Lys Leu Ser  
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val  
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
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<220>  
<223> phiYFP-M1 mutant of the phiYFP

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Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys  
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys  
 35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
 50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
 65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile  
 85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe  
 100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
 115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
 130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
 145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
 165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
 180 185 190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser  
 195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val  
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Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
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<210> 9  
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<220>  
 <223> humanized version of the phiYFP-M1

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 35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
 50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
 65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile  
 85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe  
 100 105 110



Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
 115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
 130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
 145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
 165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
 180 185 190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser  
 195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val  
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Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
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Val Ile Leu Gly Ala Met Thr Glu Thr Phe Gln Lys Lys Leu Pro Tyr  
 35 40 45

Lys Leu Glu Leu Asp Gly Asp Val Asp Gly Gln Thr Phe Lys Val Ile  
 50 55 60

Gly Glu Gly Val Gly Asp Ala Thr Thr Gly Val Ile Glu Gly Lys Tyr  
 65 70 75 80

Val Cys Thr Glu Gly Glu Val Pro Ile Ser Trp Val Ser Leu Ile Thr  
 85 90 95

Ser Leu Ser Tyr Gly Ala Lys Cys Phe Val Arg Tyr Pro Asn Glu Ile  
 100 105 110

Asn Asp Phe Phe Lys Ser Thr Phe Pro Ser Gly Tyr His Gln Glu Arg  
 115 120 125

Lys Ile Thr Tyr Glu Asn Asp Gly Val Leu Glu Thr Ala Ala Lys Ile  
 130 135 140

Thr Met Glu Ser Gly Ala Ile Val Asn Arg Ile Asn Val Lys Gly Thr  
 145 150 155 160

Gly Phe Asp Lys Asp Gly His Val Cys Gln Lys Asn Leu Glu Ser Ser  
 165 170 175

Pro Pro Ser Thr Thr Tyr Val Val Pro Glu Gly Glu Gly Ile Arg Ile  
180 185 190

Ile Tyr Arg Asn Ile Tyr Pro Thr Lys Asp Gly His Tyr Val Val Ala  
195 200 205

Asp Thr Gln Gln Val Asn Arg Pro Ile Arg Ala Gln Gly Thr Ser Ala  
210 215 220

Ile Pro Thr Tyr His His Ile Lys Ser Lys Val Asp Leu Ser Thr Asp  
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Pro Glu Glu Asn Lys Asp His Ile Ile Ile Lys Glu Thr Asn Cys Ala  
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Phe Asp Ala Asp Phe Ser  
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35 40 45

Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile  
50 55 60

Gln Tyr Gly Glu Pro Phe Phe Ala Lys Tyr Pro Asn Gly Ile Ser His  
65 70 75 80

Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Thr Ile Asp Arg Thr Val  
85 90 95

Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu  
100 105 110

Asp Gly Thr Cys Val Ile Ser Arg Ile Thr Val Asn Cys Asp Gly Phe  
115 120 125

Gln Pro Asp Gly Pro Ile Met Lys Asp Gln Leu Val Asp Ile Leu Pro  
130 135 140

Thr Glu Thr His Met Phe Pro His Gly Ser Asn Ala Val Arg Gln Leu  
145 150 155 160

Cys Tyr Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His  
165 170 175

Phe Asp Ser Lys Leu Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro  
180 185 190

Gly Pro His Phe Val Thr Val Ile Ile Lys Gln Met Lys Asp Thr Ser  
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Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser  
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Val Pro Arg Ile Thr Ser Ala Ile  
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<210> 15  
 <211> 699  
 <212> DNA  
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 Anthomedusa

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 Anthomedusae

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Phe Ile Asp Gly Val Val Asn Gly Gln Lys Phe Thr Ile Val Ala Asp  
 20 25 30

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Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys  
35 40 45

Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile  
50 55 60

Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His  
65 70 75 80

Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val  
85 90 95

Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu  
100 105 110

Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe  
115 120 125

Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro  
130 135 140

Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu  
145 150 155 160

Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His  
165 170 175

Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro  
180 185 190

Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser  
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Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser  
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Val Pro Arg Ile Thr Ser Ala Ile  
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<223> phiYFP-M1G1 mutant, derived from humanized version of the  
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<400> 17

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Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys  
 35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
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Ser Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
 65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile  
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Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe  
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Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
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Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
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Pro His Cys Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
180 185 190

Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser  
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val  
210 215 220

Arg Ala Val Asp Cys Arg Thr Ala Tyr Leu  
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Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys  
 35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
 50 55 60

Ser Trp Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
 65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile  
 85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe  
 100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Lys Gly Gln Gly Phe  
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Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
 130 135 140

Pro His Tyr Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
 145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
 165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
 180 185 190

Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser  
 195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Leu  
 210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
 225 230

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<400> 22

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Phe Ile Asp Gly Val Val Asn Gly Gln Lys Phe Thr Ile Val Ala Asp  
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35 40 45

Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile  
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Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His  
65 70 75 80

Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val  
85 90 95

Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu  
100 105 110

Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe  
115 120 125

Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro  
130 135 140

Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu  
145 150 155 160

Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His  
165 170 175

Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro  
180 185 190

Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser  
195 200 205

Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser  
210 215 220

Val Pro Arg Ile Thr Ser Ala Ile  
225 230